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RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/917,410

TIME: 11:25:55

Input Set : N:\Crf3\RULE60\09917410.raw

Output Set: N:\CRF3\01032002\I917410.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
6 CO, Man S.

8 (ii) TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
9 MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
10 PREVENTION OF ACUTE ORGAN DAMAGE AFTER
11 EXTRACORPOREAL BLOOD CIRCULATION

13 (iii) NUMBER OF SEQUENCES: 6

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Felfe & Lynch

17 (B) STREET: 805 Third Avenue

18 (C) CITY: New York

19 (D) STATE: New York

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 10022

ENTERED

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: 3.5" Computer Disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: ASCII, WordPerfect 5.1

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/917,410

C--> 31 (B) FILING DATE: 26-Jul-2001

32 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/578,953

36 (B) FILING DATE:

39 (A) APPLICATION NUMBER: EP 95 114 969.9

40 (B) FILING DATE: 19-Sep-95

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Hanson, Norman D.

44 (B) REGISTRATION NUMBER: 30,946

45 (C) REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: (212) 688-9200

49 (B) TELEFAX: (212) 838-3884

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 654 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

60 (ix) FEATURE:

61 (A) NAME/KEY: CDS

62 (B) LOCATION: 1,,654

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64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66 GAC ATT CAG ATG ACC CAA TCT CCG AGC TCT TTG TCT GCG TCT GTA GGG 48
67 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
68 1      5      10      15
70 GAT AGG GTC ACT ATC ACC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT 96
71 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
72      20      25      30
74 GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA GGA AAG GCA CCC 144
75 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
76      35      40      45
78 AAG CTT CTC ATC TAT GCT GCA TCC AAC CTA GAA TCT GGT ATC CCA TCC 192
79 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser
80      50      55      60
82 AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC ACC ATC TCT 240
83 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
84 65      70      75      80
86 TCT CTG CAG CCG GAG GAT TTC GCA ACC TAT TAC TGT CAG CAA AGT AAT 288
87 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
88      85      90      95
90 GAA GAT CCG TGG ACG TTC GGT CAA GGC ACC AAG GTG GAA ATC AAA CGA 336
91 Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
92      100      105      110
94 ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG 384
95 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
96      115      120      125
98 TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 432
99 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
100      130      135      140
102 CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG 480
103 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
104 145      150      155      160
106 GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC 528
107 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
108      165      170      175
110 TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 576
111 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
112      180      185      190
114 CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 624
115 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
116      195      200      205
118 GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT 654
119 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
120      210      215
124 (2) INFORMATION FOR SEQ ID NO: 2:
126      (i) SEQUENCE CHARACTERISTICS:
127          (A) LENGTH: 218
128          (B) TYPE: amino acid
129          (C) STRANDEDNESS: single
130          (D) TOPOLOGY: linear

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132      (ii) MOLECULE TYPE: protein
134      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
136 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
137   1           5           10           15
139 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
140           20           25           30
142 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
143           35           40           45
145 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser
146           50           55           60
148 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
149   65           70           75           80
151 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
152           85           90           95
154 Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
155           100          105          110
157 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
158           115          120          125
160 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
161           130          135          140
163 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
164 145           150          155          160
166 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
167           165          170          175
169 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
170           180          185          190
172 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
173           195          200          205
175 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
176           210          215
180 (2) INFORMATION FOR SEQ ID NO: 3:
182      (i) SEQUENCE CHARACTERISTICS:
183          (A) LENGTH: 1329 base pairs
184          (B) TYPE: nucleic acid
185          (C) STRANDEDNESS: double
186          (D) TOPOLOGY: linear
188      (ii) MOLECULE TYPE: cDNA
190      (ix) FEATURE:
191          (A) NAME/KEY: CDS
192          (B) LOCATION:1,,1329
194      (ix) FEATURE:
195          (A) NAME/KEY: mat_peptide
196          (B) LOCATION:1
198      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
200 GAA GTG CAA CTG GTG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGA 48
201 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
202   1           5           10           15
204 AGC TTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT ACC TAT 96
205 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

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206		20		25		30	
208	GCC ATG TCT TGG GTT CGC CAG GCT CCA GGG AAG GGA CTC GAG TGG GTC	144					
209	Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val						
210	35 40 45						
212	GCA TCC ATT AGT ACT GGT GGT AGC ACC TAC TAT CCA GAC AGT GTG AAG	192					
213	Ala Ser Ile Ser Thr Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys						
214	50 55 60						
216	GGC CGA TTC ACC ATC TCC AGA GAT AAT GCC AAG AAC ACC CTG TAC CTG	240					
217	Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu						
218	65 70 75 80						
220	CAA ATG AAT TCT CTG AGG GCT GAG GAC ACG GCC GTG TAT TAC TGT GCA	288					
221	Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala						
222	85 90 95						
224	AGA GAC TAT GAC GGG TAT TTT GAC TAC TGG GGC CAA GGC ACC CTG GTC	336					
225	Arg Asp Tyr Asp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val						
226	100 105 110						
228	ACA GTC TCC TCA GCT TCC ACC AAG GGC CCA TCC GTC TTC CCC CTG GCG	384					
229	Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala						
230	115 120 125						
232	CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC TGC CTG	432					
233	Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu						
234	130 135 140						
236	GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC	480					
237	Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly						
238	145 150 155 160						
240	GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA	528					
241	Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser						
242	165 170 175						
244	GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG	576					
245	Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu						
246	180 185 190						
248	GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC AGC AAC ACC	624					
249	Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr						
250	195 200 205						
252	AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA	672					
253	Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser						
254	210 215 220						
256	TGC CCA GCA CCT GAG TTC CTG GGG GGA CCA TCA GTC TTC CTG TTC CCC	720					
257	Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro						
258	225 230 235 240						
260	CCA AAA CCC AAG GAC ACT CTC ATG ATC TCC CGG ACC CCT GAG GTC ACG	768					
261	Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr						
262	245 250 255						
265	TGC GTG GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG GTC CAG TTC AAC	816					
266	Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn						
267	260 265 270						
269	TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG	864					
270	Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg						
271	275 280 285						

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273 GAG GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC 912
274 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
275      290      295      300
277 CTG CAC CAG GAC TGG CTG AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC 960
278 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
279 305      310      315      320
281 AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC ATC TCC AAA GCC AAA 1008
282 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
283      325      330      335
285 GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG 1056
286 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
287      340      345      350
289 GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC 1104
290 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
291      355      360      365
293 TAC CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG 1152
294 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
295      370      375      380
297 AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC 1200
298 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
299 385      390      395      400
301 TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG GGG 1248
302 Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
303      405      410      415
305 AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC 1296
306 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
307      420      425      430
309 ACA CAG AAG AGC CTC TCC CTG TCT CTG GGT AAA 1329
310 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
311      435      440
317 (2) INFORMATION FOR SEQ ID NO: 4:
319 (i) SEQUENCE CHARACTERISTICS:
320 (A) LENGTH: 443
321 (B) TYPE: amino acid
322 (C) STRANDEDNESS: double
323 (D) TOPOLOGY: linear
325 (ii) MOLECULE TYPE: protein
327 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
329 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
330 1      5      10      15
332 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
333      20      25      30
335 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
336      35      40      45
338 Ala Ser Ile Ser Thr Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
339      50      55      60
341 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
342 65      70      75      80
344 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

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VERIFICATION SUMMARY

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TIME: 11:25:56

Input Set : N:\Crf3\RULE60\09917410.raw

Output Set: N:\CRF3\01032002\I917410.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]